

JF4

SEQUENCE LISTING

<110> TransMIT Gesellschaft für Technologietransfer mbH
TransMIT Gesellschaft für Technologietransfer mbH

<120> Method for screening the allelic state at the 5'-flanking region of the
αS1 casein gene

<130> An127/Pri

<140> PCT/DE 03/02747
<141> 2003-08-15

<150> DE 102 38 433 A1
<151> 2002-08-16

<160> 8

<170> PatentIn version 3.1

<210> 1
<211> 18
<212> DNA
<213> Bos spec.

<220>
<221> Primer 2
<222> (1)...(18)
<223> 18 basepair, single stranded nucleic acid (linear)

<400> 1
gaagaagcag caagctgg

18

<210> 2
<211> 19
<212> DNA
<213> Bos spec.

<220>
<221> Primer 3
<222> (1)...(19)
<223> 19 basepair, single stranded nucleic acid (linear)

<400> 2
ccttgaata ttctaccag

19

<210> 3
<211> 1061
<212> DNA
<213> Bos taurus

<220>
<221> alpha-S1Kaseingen

<222> (1)..(1061)
 <223> start Exon 1 at position 620

<300>
 <301> Koczan Dirk, Hobom Gerd, Seyfert Hans-Martin
 <302> Genomic organization of the bovine alpha S1-casein gene
 <303> Nucleic acids research
 <304> 19
 <305> 20
 <306> 5591
 <307> 1991-09-24
 <308> X59856
 <309> 1991-07-18
 <313> (1)..(1061)

<300>
 <308> EMBL X59856
 <309> 1991-07-18
 <313> (1)..(1061)

<400> 3

gaatgaatga	actagttacc	acaactagta	cacccaaaat	gaacaaaaaa	tagcttggtg	60
gtataattaa	aatgccacca	aaatttatac	aataattata	tttcttttt	gcagggaaaa	120
gattagacca	catataatgt	aacttatttc	acaaggtaaa	taattataat	aaataatatg	180
gattaactga	gtttaaaag	gtgaaataaa	taatgaattc	ttctcatggt	cttgtatgtt	240
aataaaaatt	gaaaaatttt	gaagacccc	tttgcacca	agaatttcat	ttacaggtat	300
tgaattttc	aaaggttaca	aaggaaattt	tattgatata	ataaatgcat	gttctcataa	360
taaccataaa	tctagggtt	tgtggggtt	ttttttgtt	tgttaattt	gaacaatgcc	420
attccatttc	ctgtataatg	agtcaattct	ttgttgtaaa	ctctcccttag	aatttcttgg	480
gagaggaact	gaacagaaca	ttgatttcct	atgtgagaga	attcttagaa	tttaaataaa	540
cctgttggtt	aaactgaaac	cacaaaatta	gcattttact	aatcagtagg	tttaaatagc	600
ttggaagcaa	aagtctgcc	tcaccttgat	catcaaccc	gcttgctgct	tcttcccagt	660
cttgggttca	aggtattatg	tatacatata	acaaaatttc	tatgattttc	ctctgtctca	720
tcttcattc	ttcactaata	cgcagttgta	actttctat	gtgattgcaa	gtattggtag	780
tttcctatga	tatactgtta	gctaaaaat	atattgcaa	atgttgatac	tatctatctc	840
agagctatag	gtgaaaattt	aaatactttt	ataaagacca	aattgatcat	ttttaaacga	900
aattcttata	tactgaaaat	gtagatacat	aacttcagta	tagatttatg	gtaaaataat	960
ttgaatcatt	tttgtcaaat	tctgtaaaaa	gttgtcatac	agaataattt	ataatattt	1020
tgttttcata	gaaataacat	ttctggtaga	atatttcaag	g		1061

<210> 4
 <211> 652
 <212> DNA
 <213> Bos taurus

 <220>
 <221> CSN1S1-gene, 5`flanking region from position 616 and Exon 1 at position 617
 <222> (1)..(652)
 <223> Mutation/SNP position 83 (A to G), position 98 (A to G), position 298 (A to C), position 442 (A to G; change/loss of YY1- and AP1 -bindingsite), position 541 (G to A); deletion TT between position 389 and 394 compaired with Allel2

<400> 4	
gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg	60
gtataattaa aatgccacca aagtttatac aataattgta ttttctttt gcaggaaaaa	120
gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg	180
gattaactga gtttaaaag gtgaaataaa taatgaattc ttctcatggc cttgtatgtt	240
aataaaaatt gaaaaatttt gaagaccca tttgtccc agaatttcct ttacaggtat	300
tgaattttc aaaggttaca aaggaaattt tattgatata ataaatgcat gttctcataa	360
taaccataaa tctagggttt tggtgggtt ttttgttgc taattttagaa caatgccatt	420
ccatttcctg tataatgagt cgcttctttg ttgtaaactc tccttagaat ttcttggag	480
aggaactgaa cagaacattt atttcctatg tgagagaatt cttagaattt aaataaacct	540
attggttaaa ctgaaaccac aaaatttagca ttttactaat cagtaggttt aaatagcttgc	600
gaagcaaaag tctgccatca ctttgatcat caacccagct tgctgtttc tt	652

<210> 5
 <211> 654
 <212> DNA
 <213> Bos taurus

 <220>
 <221> CSN1S1-gene, 5`flanking region and Exon 1
 <222> (1)..(654)
 <223> Bindingsite for transcriptionfactor AP-1 at position 438 to 445
 Bindingsite for transcriptionfactor YY-1 at position 443 to 448

<400> 5	
gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg	60
gtataattaa aatgccacca aaatttatac aataattata ttttctttt gcaggaaaaa	120

gattagacca	catataatgt	aacttatttc	acaaggtaaa	taattataat	aaataatatg	180
gattaactga	gtttaaaag	gtgaaataaa	taatgaattc	ttctcatgg	cttgtatgtt	240
aataaaaatt	gaaaaatttt	gaagaccca	tttgc	agaatttcat	ttacaggtat	300
tgaattttc	aaaggta	aaggaaattt	tattgatata	ataaatgcat	gttctcataa	360
taaccataaa	tctagggtt	tgtgggtt	tttttg	gttaatttag	aacaatgcca	420
ttccatttcc	tgtataatga	gtcacttctt	tgtgtaaac	tctccttaga	at	480
agaggaactg	aacagaacat	tgatttccta	tgtgagagaa	ttcttaga	at	540
ctgttggta	aactgaaacc	acaaaattag	catttacta	atcagtaggt	ttaaataaac	600
tggaagcaaa	agtctgccat	cacccat	atcaacccag	cttgctgctt	tctt	654

<210> 6
 <211> 650
 <212> DNA
 <213> Bos taurus

<220>
 <221> CSN1S1-gene, 5`flanking region
 <222> (1)..(650)
 <223> Bindingsite for transcriptionfactor AP-1 at position 434 to 441
 Bindingsite for transcriptionfactor YY-1 at position 439 to 444
 deletion G and TTT between 390 and 396 compaired with Allel 2

<400> 6	gaatgaatga	actagttacc	acaactagta	cacccaaat	gaacaaaaaa	tagctgg	60
	gtataattaa	aatgccacca	aaatttatac	aataattata	tttctttt	gcagaaaaaa	120
	gattagacca	catataatgt	aacttatttc	acaaggtaaa	taattataat	aaataatatg	180
	gattaactga	gtttaaaag	gtgaaataaa	taatgaattc	ttctcatgg	cttgtatgtt	240
	aataaaaatt	gaaaaatttt	gaagaccca	tttgc	agaatttcat	ttacaggtat	300
	tgaattttc	aaaggta	aaggaaattt	tattgatata	ataaatgcat	gttctcataa	360
	taaccataaa	tctagggtt	tgtgggtt	tttttg	gttaatttag	aacaatgcca	420
	at	ttccatttcc	tgtataatga	gtcacttctt	tgtgtaaac	tctccttaga	480
	at	ctgttggta	aactgaaacc	acaaaattag	catttacta	atcagtaggt	540
	gaactgaaca	gaacattgat	ttcctatgt	agagaattct	tagaattaa	at	600
	tggttaact	gaaaccacaa	aatttcatt	ttactaatca	gtaggtttaa	at	650
	agcaaaagtc	tgccatcacc	ttgatcatca	acccagctt	ctgcttctt		

<210> 7
 <211> 650
 <212> DNA
 <213> Bos taurus

 <220>
 <221> CSN1S1-gene, 5`flanking region
 <222> (1)..(650)
 <223> Bindingsite for transcriptionfactors: AP-1 at position 434 to 441,
 , ABF1 at position 469 to 483, YY-1 at position 439 to 444;
 mutation (SNP) at position 480 (G to C), developing a ABF1-bindin
 gsite;
 deletion G and TTT between position 390 and 396 compaired with Al
 lel 2

<400> 7	
gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg	60
gtataattaa aatgccacca aaatttatac aataattata ttttcttttt gcagggaaaa	120
gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg	180
gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggc cttgtatgtt	240
aataaaaattt gaaaaattttt gaagacccc a ttttgtccca agaatttcat ttacaggtat	300
tgaatttttc aaaggtaaca aaggaaattt tattgatata ataaatgcat gttctcataa	360
taaccataaa tctagggttt tggtggggtt tttttgtta atttagaaca atgcattcc	420
atttcctgta taatgagtca cttctttgtt gtaaactctc cttagaattt cttggagac	480
gaactgaaca gaacattgat ttcctatgtg agagaattct tagaatttaa ataaacctgt	540
tggtaaact gaaaccacaa aattagcatt ttactaatca gtaggtttaa atagcttggg	600
agcaaaaatgc tgccatcacc ttgatcatca acccagctt cttgtttctt	650

<210> 8
 <211> 20
 <212> DNA
 <213> Bos spec.

 <220>
 <221> Primer1
 <222> (1)..(20)
 <223> 20 basepair, single stranded nucleic acid (linear)

<400> 8	
gaatgaatga actagttacc	20